Figure 2 shows the base sequence of cDNA containing the human UCP-2 promoter region cloned in Example 1 (continued from Figure 1 to Figure 2).

Figure 3 shows the base sequence of cDNA containing the human UCP-2 promoter region cloned in Example 1 (continued from Figure 2 to Figure 4).

Figure 4 shows the base sequence of cDNA containing the human UCP-2 promoter region cloned in Example 1 (continued from Figure 3 to Figure 5).

Figure 5 shows the base sequence of cDNA containing the human UCP-2 promoter region cloned in Example 1 (continued from Figure 4 to Figure 6).

Figure 6 shows the base sequence of cDNA containing the human UCP-2 promoter region cloned in Example 1 (continued from Figure 5).

Figure 7 shows the luciferase activity measured in Example 2.

Figure 8 shows the luciferase activity measured in Example 3.

Figure 9 shows the structure of the UCP-2 promoter deficient-clones constructed in Example 4. The numbers in the Figure represent the base number starting from the transcription initiation site.

Figure 10 shows the promoter activity measured in Example 4.

BEST MODE OF EMBODIMENT OF THE INVENTION

A DNA containing the UCP-2 promoter region containing the regulator sequence of this invention may be any DNA containing the regulator sequence described below with UCP-2 promoter activity.

Specifically, a DNA of this invention may be any DNA containing the base sequence presented by position 1 to 2270 of SEQ ID NO: 1 or a part of said sequence.

A DNA of this invention may be genomic DNA, cDNA,

and synthetic DNA derived from human and other mammalian cells (e.g. hepatocytes, splenocytes, neurocytes, glial cells, pancreatic β cells, bone marrow cells, mesangium cells, Langerhans' cells, epidermal cells, epithelial cells, endothelial cells, fibroblasts, fibre cells, muscle cells, fat cells, immune cells (e.g. macrophages, T cells, B cells, natural killer cells, mast cells, neutrophils, basophils, eosinophils, monocytes), megakaryocytes, synovial cells, chondrocytes, osteocytes, osteoblasts, osteoclasts, mammary cells, and interstitial cells, or precursor cells, stem cells, or cancer cells of said cells, and any tissue in which said cells are present, for example, the brain, each region of the brain (e.g. olfactory bulbs, amygdalloidal nucleus, basal ganglia, hippocampus, thalamus, hypothalamus, cerebral cortex, medulla oblongata, cerebellum), spinal cord, pituitary gland, stomach, pancreas, kidneys, liver, gonads, thyroid gland, gallbladder, bone marrow, adrenal glands, skin, muscle, lung, digestive tract (e.g. large intestine, small intestine), blood vessels, heart, thymus, spleen, salivary glands, peripheral blood, prostate, testes, ovaries, placenta, uterus, bones, cartilages, joints, and skeletal muscles.

Specifically, a recombinant DNA containing the human UCP-2 promoter region of this invention can be obtained as follows.

Using the base sequence corresponding to the previously reported amino acid sequences of human UCP cDNA (Fleury, C. et al. (1997), Nature Genet. Vol. 15, 269-272) as the probes, for example, human genomic library inserted in EMBL3 vector is screened by publicly known method, and λ phage clones that react with the probes are obtained. A DNA is extracted from these phage clones, and the restriction enzyme map of

the human gene inserted in the clones is prepared. DNA fragments are prepared by digestion with restriction enzymes, and the fragments react with the probes for the most upstream region of the cDNA are re-cloned in vectors for animal cells such as pCD vector, cDM8 vector (Aruffo, A. and Seed, B. (1987), Proc. Natl. Acad. Sci. USA, 84, 8573-8577), and retrovirus vector (Cone, R.D. and Mulligan, R.C. (1984), Proc. Natl. Acd. Sci. USA, 81, 6349-6353), and *Escherichia coli* plasmids such as pUC vector (Vieira, J. and Messing, J. (1987), Methods in Enzymology, 153, 3-11), and pCR-blunt vector (Ausubel, F.M. et al. (1994), Current Protocols in Molecular Biology), but not limited to these vectors. The base sequences of the cloned DNA are determined, and the position of the translation initiation codon on the gene can be determined by, for example, comparing the base sequence with the cDNA sequence. The position of the transcriptional initiation site on the gene can also be determined by comparing the base sequence with the 5' end of known cDNA. By investigating motifs in the entire sequence, the binding site of known transcriptional regulatory factors can be determined.

The obtained DNA can be used without modification or if necessary, after digestion with restriction enzymes or being bound by linkers.

To measure the promoter activity, a detectable structural gene may be connected in downstream of the promoter region. For the structural gene connected in downstream of the promoter region, various reporter genes are used. For the reporter gene, luciferase gene, chloramphenicol acetyltransferase (CAT) gene, alkaline phosphatase gene, and β-galctosidase gene are commonly used, but any other structural genes for which a method of detecting the gene product is available may be used. To insert the above structural gene into the vector,